

SEQUENCE LISTING

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10870
<120> INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
CO-STIMULATORY ANTIGENS

<130> 37003-275681

<140> 09/576,424

<141> 2000-05-22

<150> PCT/US97/19906

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<150> 08/746,361

<151> 1996-11-08

<150> 08/487,550

<151> 1995-06-07

<160> 12

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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ggg gca cga tgt gcc tat gaa ctg act cag cca ccc tcg gtg tca gtg	96
Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val	
20 25 30	
tcc cca gga cag acg gcc agg atc acc tgt ggg gga gac aac agt aga	144
Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg	
35 40 45	
aat gaa tat gtc cac tgg tac cag cag aag cca gcg cgg gcc cct ata	192
Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile	
50 55 60	
ctg gtc atc tat gat gat agt gac cgg ccc tca ggg atc cct gag cga	240
Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg	
65 70 75 80	

ttc tct ggc tcc aaa tca ggg aac acc gcc acc ctg acc atc aac ggg 288
 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
 85 90 95

gtc gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agg 336
 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
 100 105 110

gct agt gat cat ccg gtc ttc gga gga ggg acc cgg gtg acc gtc cta 384
 Ala Ser Asp His Pro Val Phe Gly Gly Thr Arg Val Thr Val Leu
 115 120 125

ggc cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct 432
 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 130 135 140

gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac 480
 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 145 150 155 160

ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc 528
 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 165 170 175

gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac 576
 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 180 185 190

aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag 624
 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 195 200 205

tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg 672
 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
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 <213> Homo sapiens

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Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
 35 40 45

Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
50 55 60

Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
65 70 75 80

Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
85 90 95

Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
100 105 110

Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
115 120 125

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
130 135 140

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
145 150 155 160

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
165 170 175

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
180 185 190

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
195 200 205

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
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Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
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<212> DNA

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gtc ctg tcc cag gtg aag ctg cag cag tgg ggc gaa gga ctt ctg cag 96
Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
20 25 30

cct tcg gag acc ctg tcc cgc acc tgc gtt gtc tct ggt ggc tcc atc 144
Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
35 40 45

agc ggt tac tac tac tgg acc tgg atc cgc cag acc cca ggg agg gga 192
 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
 50 55 60

ctg gag tgg att ggc cat att tat ggt aat ggt gcg acc acc aac tac 240
 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
 65 70 75 80

aat ccc tcc ctc aag agt cga gtc acc att tca aaa gac acg tcc aag 288
 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
 85 90 95

aac cag ttc ttc ctg aac ttg aat tct gtg acc gac gcg gac acg gcc 336
 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
 100 105 110

gtc tat tac tgt gcg aga ggc cct cgc cct gat tgc aca acc att tgt 384
 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
 115 120 125

tat ggc ggc tgg gtc gat gtc tgg ggc ccg gga gac ctg gtc acc gtc 432
 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
 130 135 140

tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 480
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 145 150 155 160

tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag 528
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 165 170 175

gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg 576
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 180 185 190

acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc 624
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 195 200 205

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc 672
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 210 215 220

cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg 720
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 225 230 235 240

gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca tgc cca 768
 Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 245 250 255

ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc 816
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 260 265 270

ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc 864
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 275 280 285

aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc 912
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 290 295 300

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg 960
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 305 310 315 320

cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc 1008
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 325 330 335

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc 1056
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 340 345 350

tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc 1104
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 355 360 365

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg 1152
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 370 375 380

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 1200
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 1248
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 1296
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 420 425 430

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1344
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 435 440 445

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1392
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1431
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 465 470 475

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Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
 35 40 45

Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
 50 55 60

Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
 65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
 85 90 95

Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
 115 120 125

Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
 130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 145 150 155 160

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 165 170 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 180 185 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 195 200 205

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 210 215 220

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 225 230 235 240

Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 245 250 255

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 260 265 270

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 275 280 285

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 290 295 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 305 310 315 320
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 325 330 335
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 340 345 350
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 355 360 365
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 370 375 380
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 420 425 430
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
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 ggg tcc agt ggg gaa gtt gtg atg act cag tct cca ctg tcc ctt ccc 96
 Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30
 atc aca cct gga gag ccg gcc tcc atc tcc tgt agg tct agt caa agc 144
 Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45

ctt aaa cac agt aat gga gac acc ttc ctg agt tgg tat cag cag aag 192
 Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys
 50 55 60

cca ggc caa cct cca agg ctc ctg att tat aag gtt tct aac cgg gac 240
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp
 65 70 75 80

tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gat ttc 288
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
 85 90 95

aca ctg aaa atc agc gca gtg gag gct gaa gat gtt ggg gtt tat ttc 336
 Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe
 100 105 110

tgc ggg caa ggt aca agg act cct ccc act ttc ggc gga ggg acc aag 384
 Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys
 115 120 125

gtg gaa atc aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg 432
 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 130 135 140

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 145 150 155 160

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 165 170 175

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga 720
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 225 230 235

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<211> 239

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<213> Homo sapiens

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20 25 30

Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
85 90 95

Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe
100 105 110

Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<211> 1437

<212> DNA

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48

D2
CONT.

gtc cag tgt gag gtg caa ctg gtg gag tct ggg gga ggc ttg gtc cag 96
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cct ggc ggg tcc ctg aga gtc tcc tgt gca gtc tct gga ttc acc ttc 144
 Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45

agt gac cac tac atg tat tgg ttc cgc cag gct cca ggg aag ggg ccg 192
 Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro
 50 55 60

gaa tgg gta ggt ttc att aga aac aaa ccg aac ggt ggg aca aca gaa 240
 Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu
 65 70 75 80

tac gcc gcg tct gtg aaa gac aga ttc acc atc tcc aga gat gat tcc 288
 Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95

aaa agc atc gcc tat ctg caa atg agc agc ctg aaa atc gag gac acg 336
 Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr
 100 105 110

gcc gtc tat tac tgt act aca tcc tac att tca cat tgt cgg ggt ggt 384
 Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly
 115 120 125

gtc tgc tat gga ggt tac ttc gaa ttc tgg ggc cag ggc gcc ctg gtc 432
 Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val
 130 135 140

acc gtc tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca 480
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 145 150 155 160

ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg 528
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 165 170 175

gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc 576
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 180 185 190

gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca 624
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 195 200 205

gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg 672
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 210 215 220

ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc 720
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 225 230 235 240

Dr.
CONF.

aag gtg gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca 768
 Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 245 250 255

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc 816
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 260 265 270

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct 864
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 275 280 285

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc 912
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 290 295 300

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca 960
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 305 310 315 320

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc 1008
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 325 330 335

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc 1056
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 340 345 350

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc 1104
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 355 360 365

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 1152
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 370 375 380

tcc ccg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc 1200
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg 1248
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 405 410 415

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac 1296
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg 1344
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 435 440 445

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1392
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 450 455 460

DZ
cont.

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Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45

Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro
 50 55 60

Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu
 65 70 75 80

Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95

Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr
 100 105 110

Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly
 115 120 125

Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val
 130 135 140

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 145 150 155 160

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 165 170 175

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 180 185 190

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 195 200 205

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 210 215 220

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 225 230 235 240

Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 245 250 255

D2
 cont.

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 9

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(708)

<400> 9

atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca 48
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

ggt gca cga tgt gag tct gtc ctg aca cag ccg ccc tca gtg tct ggg	96
Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly	
20 25 30	
gcc cca ggg cag aag gtc acc atc tcg tgc act ggg agc acc tcc aac	144
Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn	
35 40 45	
att gga ggt tat gat cta cat tgg tac cag cag ctc cca gga acg gcc	192
Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala	
50 55 60	
ccc aaa ctc ctc atc tat gac att aac aag cga ccc tca gga att tct	240
Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser	
65 70 75 80	
gac cga ttc tct ggc tcc aag tct ggt acc gcg gcc tcc ctg gcc atc	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile	
85 90 95	
act ggg ctc cag act gag gat gag gct gat tat tac tgc cag tcc tat	336
Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr	
100 105 110	
gac agc agc ctg aat gct cag gta ttc gga gga ggg acc cgg ctg acc	384
Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr	
115 120 125	
gtc cta ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc	432
Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro	
130 135 140	
tcc tct gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata	480
Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile	
145 150 155 160	
agt gac ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc	528
Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser	
165 170 175	
agc ccc gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc	576
Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser	
180 185 190	
aac aac aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag	624
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln	
195 200 205	
tgg aag tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc	672
Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser	
210 215 220	
acc gtg gag aag aca gtg gcc cct aca gaa tgt tca tga	711
Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser	
225 230 235	

Dr
CONT.

<210> 10
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly
 20 25 30

Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn
 35 40 45

Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 50 55 60

Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser
 65 70 75 80

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile
 85 90 95

Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
 100 105 110

Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr
 115 120 125

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
 130 135 140

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
 145 150 155 160

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
 165 170 175

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
 180 185 190

Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
 195 200 205

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
 210 215 220

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 225 230 235

<210> 11
 <211> 1431
 <212> DNA
 <213> Homo sapiens

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<220>

<221> CDS

<222> (1)..(1428)

<400> 11

atg	aaa	cac	ctg	tgg	ttc	ttc	ctc	ctc	ctg	gtg	gca	gct	ccc	aga	tgg	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		
gtc	ctg	tcc	cag	gtg	cag	ctg	cag	gag	tcg	ggc	cca	gga	ctg	gtg	aag	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	
			20					25					30			
cct	tcg	gag	acc	ctg	tcc	ctc	acc	tgc	gct	gtc	tct	ggg	ggc	tcc	atc	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Ser	Ile	
			35				40					45				
agc	ggg	ggg	tat	ggc	tgg	ggc	tgg	atc	cgc	cag	ccc	cca	ggg	aag	ggg	192
Ser	Gly	Gly	Tyr	Gly	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	
	50					55					60					
ctg	gag	tgg	att	ggg	agt	ttc	tat	agt	agt	agt	ggg	aac	acc	tac	tac	240
Leu	Glu	Trp	Ile	Gly	Ser	Phe	Tyr	Ser	Ser	Ser	Gly	Asn	Thr	Tyr	Tyr	
	65					70				75					80	
aac	ccc	tcc	ctc	aag	agt	caa	gtc	acc	att	tca	aca	gac	acg	tcc	aag	288
Asn	Pro	Ser	Leu	Lys	Ser	Gln	Val	Thr	Ile	Ser	Thr	Asp	Thr	Ser	Lys	
				85					90					95		
aac	cag	ttc	tcc	ctg	aag	ctg	aac	tct	atg	acc	gcc	gcg	gac	acg	gcc	336
Asn	Gln	Phe	Ser	Leu	Lys	Leu	Asn	Ser	Met	Thr	Ala	Ala	Asp	Thr	Ala	
			100					105					110			
gtg	tat	tac	tgt	gtg	aga	gat	cgt	ctt	ttt	tca	gtt	gtt	gga	atg	gtt	384
Val	Tyr	Tyr	Cys	Val	Arg	Asp	Arg	Leu	Phe	Ser	Val	Val	Gly	Met	Val	
			115				120						125			
tac	aac	aac	tgg	ttc	gat	gtc	tgg	ggc	ccg	gga	gtc	ctg	gtc	acc	gtc	432
Tyr	Asn	Asn	Trp	Phe	Asp	Val	Trp	Gly	Pro	Gly	Val	Leu	Val	Thr	Val	
	130					135					140					
tcc	tca	gct	agc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	480
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
			145			150				155					160	
tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	528
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
				165					170					175		
gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	576
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
			180					185					190			
acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	624
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
			195				200					205				

D2
CONT.

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	672
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
225 230 235 240	
gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca tgc cca	768
Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
245 250 255	
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc	816
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	
260 265 270	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	864
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
275 280 285	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	912
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
290 295 300	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	960
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
305 310 315 320	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	1008
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
325 330 335	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1056
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
340 345 350	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1104
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
355 360 365	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1152
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
370 375 380	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1200
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
385 390 395 400	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1248
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
405 410 415	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1296
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
420 425 430	

or
cont.

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1344
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 435 440 445

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1392
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 450 455 460

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1431
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

<210> 12

<211> 476

<212> PRT

<213> Homo sapiens

<400> 12

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile
 35 40 45

Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr
 65 70 75 80

Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys
 85 90 95

Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val
 115 120 125

Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val
 130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 145 150 155 160

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 165 170 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 180 185 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 195 200 205

22
cont.

Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	210	215	220	
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	225	230	235	240
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	245	250	255	
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	260	265	270	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	275	280	285	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	290	295	300	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	305	310	315	320
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	325	330	335	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	340	345	350	
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	355	360	365	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	370	375	380	
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	385	390	395	400
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	405	410	415	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	420	425	430	
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	435	440	445	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	450	455	460	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	465	470	475					

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 210 215 220
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 225 230 235 240
 Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 245 250 255
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 260 265 270
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 275 280 285
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 290 295 300
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 305 310 315 320
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 325 330 335
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 340 345 350
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 355 360 365
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 370 375 380
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 420 425 430
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 435 440 445
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 450 455 460
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

B2
 cont.